Amendments to the Claims:

1. (Currently Amended) A polynucleotide fragment comprising a polynucleotide sequence encoding a polypeptide having heparanase catalytic activity, wherein said polypeptide shares at least 70% homology with SEQ ID NOs:10, ~~14 or 44~~, as determined using default parameters of a DNA sequence analysis software package developed by the Genetic Computer Group (GCG) at the University of Wisconsin.

2. (Original) The polynucleotide fragment of claim 1, wherein said polynucleotide sequence includes nucleotides 63-1691 of SEQ ID NO:9.

3. (Original) The polynucleotide fragment of claim 1, wherein said polynucleotide sequence includes nucleotides 63-721 of SEQ ID NO:9.

4. (Original) The polynucleotide fragment of claim 1, wherein said polynucleotide is as set forth in SEQ ID NO:9.

5. (Original) The polynucleotide fragment of claim 1, wherein said polynucleotide sequence includes a segment of SEQ ID NO:9, said segment encodes said polypeptide having said heparanase catalytic activity.

6. (Currently Amended) The polynucleotide fragment of claim 1, wherein said polypeptide includes an amino acid sequence as set forth in SEQ ID NOs:10~~, 14 or 44~~.

7. (Currently Amended) The polynucleotide fragment of claim 1, wherein said polypeptide includes a segment of SEQ ID NOs:10, ~~14 or 44~~ said segment harbors said heparanase catalytic activity.

8. (Original) The polynucleotide fragment of claim 1, wherein said polynucleotide sequence is selected from the group consisting of double stranded DNA, single stranded DNA and RNA.

9. (currently amended) A polynucleotide sequence as set forth in SEQ ID NOs:9~~, 13, 42 or~~ 43.

10. (Currently Amended) A polynucleotide sequence at least 70% homologous to SEQ ID NOs:9, ~~13, 42 or 43~~, as determined using default parameters of a DNA sequence analysis software package developed by the Genetic Computer Group (GCG) at the University of Wisconsin, wherein said polynucleotide sequence encodes a polypeptide having heparanase catalytic activity.

11. (Currently Amended) A vector comprising a polynucleotide sequence encoding a polypeptide having heparanase catalytic activity, wherein said polypeptide shares 70% homology with SEQ ID NOs:10, ~~14 or 44~~, as determined using default parameters of a DNA sequence analysis software package developed by the Genetic Computer Group (GCG) at the University of Wisconsin.

12. (Original) The vector of claim 11, wherein said polynucleotide sequence includes nucleotides 63-1691 of SEQ ID NO:9.

13. (Original) The vector of claim 11, wherein said polynucleotide sequence includes nucleotides 63-721 of SEQ ID NO:9.

14. (Original) The vector of claim 11, wherein said polynucleotide sequence is as set forth in SEQ ID NO:9.

15. (Original) The vector of claim 11, wherein said polynucleotide sequence includes a segment of SEQ ID NO:9, said segment encodes said polypeptide having said heparanase catalytic activity.

16. (Currently Amended) The vector of claim 11, wherein said polypeptide includes an amino acid sequence as set forth in SEQ ID NOs:10, ~~14 or 44~~.

17. (Currently Amended) The vector of claim 11, wherein said polypeptide includes a segment of SEQ ID NOs:10, ~~14 or 44~~, said segment harbors said heparanase catalytic activity.

18. (Original) The vector of claim 11, wherein said polynucleotide sequence is selected from the group consisting of double stranded DNA, single stranded DNA and RNA.

19. (Original) The vector of claim 11, wherein said vector is a baculovirus vector.

20. (Currently Amended) A host cell comprising an exogenous polynucleotide fragment including a polynucleotide sequence encoding a polypeptide having heparanase catalytic activity, wherein said polypeptide shares 70% homology with SEQ ID NOs:10~~, 14 or 44~~, as determined using default parameters of a DNA sequence analysis software package developed by the Genetic Computer Group (GCG) at the University of Wisconsin.

21. (Original) The host cell of claim 20, wherein said polynucleotide sequence includes nucleotides 63-1691 of SEQ ID NO:9.

22. (Original) The host cell of claim 20, wherein said polynucleotide sequence includes nucleotides 63-721 of SEQ ID NO:9.

23. (Original) The host cell of claim 20, wherein said polynucleotide sequence is as set forth in SEQ ID NO:9.

24. (Original) The host cell of claim 20, wherein said polynucleotide sequence includes a segment of SEQ ID NO:9, said segment encodes said polypeptide having said heparanase catalytic activity.

25. (Currently Amended) The host cell of claim 20, wherein said polypeptide includes an amino acid sequence as set forth in SEQ ID NOs:10~~, 14 or 44~~.

26. (Currently Amended) The host cell of claim 20, wherein said polypeptide includes a segment of SEQ ID NOs:10~~, 14 or 44~~ said segment harbors said heparanase catalytic activity.

27. (Original) The host cell of claim 20, wherein said polynucleotide sequence is selected from the group consisting of double stranded DNA, single stranded DNA and RNA.

28. (Currently Amended) A host cell expressing a recombinant heparanase, wherein said recombinant heparanase shares 70% homology with SEQ ID NOs:10~~, 14 or 44~~, as

determined using default parameter of a DNA sequence analysis software package developed by the Genetic Computer (Group (GCG) at the University of Wisconsin.

29. (Currently Amended) A heparanase overexpression system comprising a cell overexpressing heparanase catalytic activity, wherein said heparanase catalytic activity is effected by a recombinant heparanase sharing at least 70% homology with SEQ ID NOs:10, ~~14 or 44~~, as determined using default parameters of a DNA sequence analysis software package developed by the Genetic Computer Group (GCG) at the University of Wisconsin.

30. (Original) The host cell of claim 20, wherein said cell is an insect cell.

31. (New) A polynucleotide fragment comprising a polynucleotide sequence encoding a polypeptide having heparanase catalytic activity, wherein said polypeptide shares at least 70% homology with SEQ ID NO:10 as determined using default parameters of a DNA sequence analysis software package developed by the Genetic Computer Group (GCG) at the University of Wisconsin, wherein said polypeptide is characterized by being about 50 or about 65 kDa, and said polypeptide is characterized by being capable of being purified with a purification procedure initiated with Heparin-Sepharose chromatography, followed by gel filtration and pooling of active column fractions, wherein a quantity of said polypeptide after said purification correlates with heparanase activity in said pooled active column fractions.